

RAW SEQUENCE LISTING

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Application Serial Number: 10/088594B
Source: FW10
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IFW16

RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/088,594B

TIME: 16:07:46

Input Set : A:\5.1198 Sequence Listing.txt

Output Set: N:\CRF4\02022005\J088594B.raw

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4 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
6 <120> TITLE OF INVENTION: Novel Transaldolase
8 <130> FILE REFERENCE: 00005.001198
10 <140> CURRENT APPLICATION NUMBER: US/10/088,594B
11 <141> CURRENT FILING DATE: 2002-03-21
13 <150> PRIOR APPLICATION NUMBER: JP 99/266548
14 <151> PRIOR FILING DATE: 1999-09-21
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1080
22 <212> TYPE: DNA
23 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
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31 gtcaccacca acccagctat ttctgcagca gcaatgtcca agggcgattc ctacgacgct 180
33 cagatcgagc agctcaaggc cgctggcgca tctgttgacc aggctgttta cgccatgagc 240
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39 ctggctcagg ccaaggagct gtgggcaaag gttgatcgtc caaacgtcat gatcaagatc 420
41 cctgcaaccc caggttcttt gccagcaatc accgacgctt tggctgaggg catcagcggt 480
43 aacgtcacct tgatcttctc cgttgctcgc taccgcgagg tcatcgctgc gtacatcgag 540
45 ggaatcaagc aggcagctgc aaacggccac gacgtatcca agatccactc tgtggcttcc 600
47 ttcttcgtct cccgcgtcga cgttgagatc gacaagcgcc tcgaggcaat cggatccgat 660
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51 tacaaggagc ttttcgagc cgccgagctg cctgaagggtg ccaacactca gcgccactg 780
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55 gctggtccaa acaccgtcaa caccatgcca gaaggcacca tcgacgctgt tctggaactg 900
57 ggcaacctgc acggtgacac cctgtccaac tccgcggcag aagctgacgc tgtgttctcc 960
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74 gtcaccacca acccagctat ttctgcagca gcaatgtcca agggcgattc ctacgacgct 180
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118 <222> LOCATION: (2643)..(3722)
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261 <210> SEQ ID NO: 4

262 <211> LENGTH: 360

263 <212> TYPE: PRT

264 <213> ORGANISM: Corynebacterium glutamicum ATCC31388

266 <400> SEQUENCE: 4

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275              35              40              45
277 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
278              50              55              60
280 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
281      65              70              75              80
283 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
284              85              90              95
286 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
287              100             105             110
289 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
290              115             120             125
292 Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
293              130             135             140
295 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
296      145             150             155             160
298 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala
299              165             170             175
301 Ala Tyr Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
302              180             185             190
304 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
305              195             200             205
307 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
308              210             215             220
310 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
311      225             230             235             240
313 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
314              245             250             255
316 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
317              260             265             270
319 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
320              275             280             285
322 Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His
323              290             295             300
325 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
326      305             310             315             320
328 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
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337 <210> SEQ ID NO: 5
338 <211> LENGTH: 700
339 <212> TYPE: PRT
340 <213> ORGANISM: Corynebacterium glutamicum ATCC31388

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342 <400> SEQUENCE: 5

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350 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
351 30           35           40           45
353 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
354           50           55           60
356 Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala
357           65           70           75
359 Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln
360           80           85           90
362 Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu
363           95           100          105
365 Lys Ala Leu Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr
366 110           115           120           125
368 Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly
369           130           135           140
371 Leu Ala Ser Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly
372           145           150           155
374 Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His
375           160           165           170
377 Ile Tyr Val Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser
378           175           180           185
380 Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val
381 190           195           200           205
383 Phe Trp Asp Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala
384           210           215           220
386 Phe Asn Glu Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr
387           225           230           235
389 Ile Glu Val Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val
390           240           245           250
392 Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg
393           255           260           265
395 Thr Ile Ile Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val
396 270           275           280           285
398 His Gly Ala Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu
399           290           295           300
401 Leu Gly Phe Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile
402           305           310           315
404 Ala His Thr Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala
405           320           325           330
407 Trp Gln Val Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys
408           335           340           345
410 Ala Leu Phe Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala
411 350           355           360           365
413 Asp Glu Leu Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg
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